

## STIC Biotechnology Systems Branch

### RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/511,530  
Source: P5/10  
Date Processed by STIC: 8/8/05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebs/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER: 10/511,530

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos     The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."
  
- 2      Invalid Line Length     The rules require that a line **not** exceed 72 characters in length. This includes white spaces.
  
- 3 ✓ Misaligned Amino  
    Numbering     The numbering under each 5<sup>th</sup> amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
  
- 4 ✓ Non-ASCII     The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**
  
- 5      Variable Length     Sequence(s)          contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
  
- 6      PatentIn 2.0  
    "bug"     A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)         . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
  
- 7      Skipped Sequences  
    (OLD RULES)     Sequence(s)          missing. If intentional, please insert the following lines for **each** skipped sequence:  
                                   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                                   (i)     SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                                   (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                                   This sequence is intentionally skipped  
  
                                   Please also adjust the "(ii) NUMBER OF SEQUENCES." response to **include** the skipped sequences.
  
- 8      Skipped Sequences  
    (NEW RULES)     Sequence(s)          missing. If **intentional**, please insert the following lines for **each** skipped sequence.  
                                   <210> sequence id number  
                                   <400> sequence id number  
                                   000
  
- 9      Use of n's or Xaa's  
    (NEW RULES)     Use of n's and/or Xaa's have been detected in the Sequence Listing.  
                                   Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.  
                                   In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
  
- 10      Invalid <213>  
    Response     Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence
  
- 11      Use of <220>     Sequence(s)          missing the <220> "Feature" and associated numeric identifiers and responses.  
                                   Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
                                   (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
  
- 12      PatentIn 2.0  
    "bug"     Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
  
- 13      Misuse of n/Xaa     "n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid



PCT

## RAW SEQUENCE LISTING

DATE: 08/08/2005

PATENT APPLICATION: US/10/511,530

TIME: 09:54:56

Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\08082005\J511530.raw

*see item 4 on  
Error summary sheet*

4 <110> APPLICANT: CEREMEDIX, INC.  
5 Adams, David S.  
6 Shashoua, Victor E.  
8 <120> TITLE OF INVENTION: PEPTIDE-DEPENDENT UPREGULATION OF TELOMERASE EXPRESSION  
W--> 9 <130> FILE REFERENCE: 6285-04US  
11 <140> CURRENT APPLICATION NUMBER: US 10/511,530  
C--> 12 <141> CURRENT FILING DATE: 2004-10-15  
14 <150> PRIOR APPLICATION NUMBER: PCT/US03/03425  
15 <151> PRIOR FILING DATE: 2003-02-03  
17 <160> NUMBER OF SEQ ID NOS: 31

## ERRORED SEQUENCES

19 <210> SEQ ID NO: 1  
20 <211> LENGTH: 12  
21 <212> TYPE: PRT  
22 <213> ORGANISM: artificial  
24 <220> FEATURE:  
25 <223> OTHER INFORMATION: upregulator of telomerase expression  
27 <400> SEQUENCE: 1  
29 Gln Tyr Lys Leu Gly Ser Lys Thr Gly Pro Gly Gln  
E--> 30 1 ~~5-10~~ 5 *10 ← mislabeled amino acid numbers - see*  
33 <210> SEQ ID NO: 2 *item 3*  
34 <211> LENGTH: 6 *on Error*  
35 <212> TYPE: PRT *summary*  
36 <213> ORGANISM: artificial *sheet*  
38 <220> FEATURE:  
39 <223> OTHER INFORMATION: upregulator of telomerase expression  
41 <400> SEQUENCE: 2  
43 Gln Thr Leu Gln Phe Arg *same error*  
E--> 44 1 ~~5~~  
46 <210> SEQ ID NO: 3  
47 <211> LENGTH: 7  
48 <212> TYPE: PRT  
49 <213> ORGANISM: artificial  
51 <220> FEATURE:  
52 <223> OTHER INFORMATION: upregulator of telomerase expression  
55 <220> FEATURE:  
W--> 56 <221> NAME/KEY: MISC FEATURE *use MISC FEATURE, instead*  
57 <222> LOCATION: (1)..(1) *↑*  
58 <223> OTHER INFORMATION: X1 is Asp or Asn *add underscore*  
60 <220> FEATURE:

## RAW SEQUENCE LISTING

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Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\08082005\J511530.raw

```

W--> 61 <221> NAME/KEY: MISC FEATURE
      62 <222> LOCATION: (3)..(3)
      63 <223> OTHER INFORMATION: X3 is Asp or Asn
W--> 64 <220> FEATURE:
W--> 65 <221> NAME/KEY: MISC FEATURE
      66 <222> LOCATION: (4)..(4)
      67 <223> OTHER INFORMATION: X4 is absent or Gly
W--> 68 <220> FEATURE:
      69 <221> NAME/KEY: MISC FEATURE
      70 <222> LOCATION: (5)..(5)
      71 <223> OTHER INFORMATION: X5 is absent, Asp, or Phe
W--> 73 <220> FEATURE:
      74 <221> NAME/KEY: MISC FEATURE
      75 <222> LOCATION: (6)..(6)
      76 <223> OTHER INFORMATION: X6 is absent, Ala, or Phe
W--> 78 <220> FEATURE:
      79 <221> NAME/KEY: MISC FEATURE
      80 <222> LOCATION: (7)..(7)
      81 <223> OTHER INFORMATION: X7 is absent or Ala
      83 <400> SEQUENCE: 3
W--> 85 Xaa Gly Xaa Xaa Xaa Xaa Xaa
E--> 86 1 5 same env
      89 <210> SEQ ID NO: 4
      90 <211> LENGTH: 5
      91 <212> TYPE: PRT
      92 <213> ORGANISM: artificial
      94 <220> FEATURE:
      95 <223> OTHER INFORMATION: upregulator of telomerase expression
      97 <400> SEQUENCE: 4
      99 Asp Gly Asp Gly Asp same
E--> 100 1 5
      103 <210> SEQ ID NO: 5
      104 <211> LENGTH: 6
      105 <212> TYPE: PRT
      106 <213> ORGANISM: artificial
      108 <220> FEATURE:
      109 <223> OTHER INFORMATION: upregulator of telomerase expression
      111 <400> SEQUENCE: 5
      113 Asp Gly Asp Gly Phe Ala same
E--> 114 1 5
      117 <210> SEQ ID NO: 6
      118 <211> LENGTH: 7
      119 <212> TYPE: PRT
      120 <213> ORGANISM: artificial
      122 <220> FEATURE:
      123 <223> OTHER INFORMATION: upregulator of telomerase expression
      125 <400> SEQUENCE: 6
      127 Asp Gly Asp Gly Asp Phe Ala
E--> 128 1 5 same

```

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Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\08082005\J511530.raw

```

131 <210> SEQ ID NO: 7
132 <211> LENGTH: 7
133 <212> TYPE: PRT
134 <213> ORGANISM: artificial
136 <220> FEATURE:
137 <223> OTHER INFORMATION: upregulator of telomerase expression
139 <400> SEQUENCE: 7
141   Asp Gly Asn Gly Asp Phe Ala
E--> 142   1 5      same
145 <210> SEQ ID NO: 8
146 <211> LENGTH: 7
147 <212> TYPE: PRT
148 <213> ORGANISM: artificial
150 <220> FEATURE:
151 <223> OTHER INFORMATION: upregulator of telomerase expression
153 <400> SEQUENCE: 8
155 Asn Gly Asn Gly Asp Phe Ala
E--> 156 1 5      same
159 <210> SEQ ID NO: 9
160 <211> LENGTH: 7
161 <212> TYPE: PRT
162 <213> ORGANISM: artificial
164 <220> FEATURE:
165 <223> OTHER INFORMATION: upregulator of telomerase expression
167 <400> SEQUENCE: 9
169 Asn Gly Asp Gly Asp Phe Ala
E--> 170 1 5      same
171 <210> SEQ ID NO: 10
172 <211> LENGTH: 8
173 <212> TYPE: PRT
174 <213> ORGANISM: artificial
176 <220> FEATURE:
177 <223> OTHER INFORMATION: upregulator of telomerase expression
180 <220> FEATURE:
181 <221> NAME/KEY: MISC_FEATURE
182 <222> LOCATION: (1)..(1)
183 <223> OTHER INFORMATION: X1 is absent or Ser
185 <220> FEATURE:
186 <221> NAME/KEY: MISC_FEATURE
187 <222> LOCATION: (2)..(2)
188 <223> OTHER INFORMATION: X2 is absent or Lys
190 <400> SEQUENCE: 10
W--> 192 Xaa Xaa Met Thr Leu Thr Gln Pro
E--> 193 1 5      same
196 <210> SEQ ID NO: 11
197 <211> LENGTH: 6
198 <212> TYPE: PRT
199 <213> ORGANISM: artificial
201 <220> FEATURE:

```

## RAW SEQUENCE LISTING

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Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\08082005\J511530.raw

202 <223> OTHER INFORMATION: upregulator of telomerase expression  
 204 <400> SEQUENCE: 11  
 206 Met Thr Leu Thr Gln Pro  
 E--> 207 1 5 *none*  
 223 <210> SEQ ID NO: 13  
 224 <211> LENGTH: 5  
 225 <212> TYPE: PRT  
 226 <213> ORGANISM: artificial  
 228 <220> FEATURE:  
 229 <223> OTHER INFORMATION: upregulator of telomerase expression  
 W--> 230 <220> FEATURE:  
 231 <221> NAME/KEY: MISC\_FEATURE  
 232 <222> LOCATION: (3)..(3)  
 233 <223> OTHER INFORMATION: X3 is Glu or Leu  
 W--> 234 <220> FEATURE:  
 235 <221> NAME/KEY: MISC\_FEATURE  
 236 <222> LOCATION: (4)..(4)  
 237 <223> OTHER INFORMATION: X4 is Ala or Glu  
 W--> 239 <220> FEATURE:  
 240 <221> NAME/KEY: MISC\_FEATURE  
 241 <222> LOCATION: (5)..(5)  
 242 <223> OTHER INFORMATION: X5 is absent, Leu, or Ala  
 244 <400> SEQUENCE: 13  
 W--> 246 Asp Gly Xaa Xaa Xaa *none*  
 E--> 247 1 5  
 264 <210> SEQ ID NO: 15  
 265 <211> LENGTH: 11  
 266 <212> TYPE: PRT  
 267 <213> ORGANISM: artificial  
 269 <220> FEATURE:  
 270 <223> OTHER INFORMATION: upregulator of telomerase expression  
 273 <220> FEATURE:  
 274 <221> NAME/KEY: MISC\_FEATURE  
 275 <222> LOCATION: (1)..(2)  
 276 <223> OTHER INFORMATION: X1 and X2 are absent or are any amino acid  
 278 <220> FEATURE:  
 279 <221> NAME/KEY: MISC\_FEATURE  
 280 <222> LOCATION: (5)..(5)  
 281 <223> OTHER INFORMATION: X5 is Glu or Leu  
 283 <220> FEATURE:  
 284 <221> NAME/KEY: MISC\_FEATURE  
 285 <222> LOCATION: (6)..{6}  
 286 <223> OTHER INFORMATION: X6 is Ala or Glu  
 288 <220> FEATURE:  
 289 <221> NAME/KEY: MISC\_FEATURE  
 290 <222> LOCATION: (7)..(7)  
 291 <223> OTHER INFORMATION: X7 is absent, Leu, or Ala  
 293 <220> FEATURE:  
 294 <221> NAME/KEY: MISC\_FEATURE

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Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\08082005\J511530.raw

```

295 <222> LOCATION: (8)..(11)
296 <223> OTHER INFORMATION: X8, X9, X10, X11 are absent or are any amino acid
298 <400> SEQUENCE: 15
W--> 300 Xaa Xaa Asp Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa
E--> 301 1 5 10 same
304 <210> SEQ ID NO: 16
305 <211> LENGTH: 5
306 <212> TYPE: PRT
307 <213> ORGANISM: artificial
309 <220> FEATURE:
310 <223> OTHER INFORMATION: upregulator of telomerase expression
312 <400> SEQUENCE: 16
314 Asp Gly Glu Ala Leu same
E--> 315 1 5
318 <210> SEQ ID NO: 17
319 <211> LENGTH: 5
320 <212> TYPE: PRT
321 <213> ORGANISM: artificial
323 <220> FEATURE:
324 <223> OTHER INFORMATION: upregulator of telomerase expression
326 <400> SEQUENCE: 17
328 Asp Gly Leu Glu Ala same
E--> 329 1 5
331 <210> SEQ ID NO: 18
332 <211> LENGTH: 6
333 <212> TYPE: PRT
334 <213> ORGANISM: artificial
336 <220> FEATURE:
337 <223> OTHER INFORMATION: upregulator of telomerase expression
339 <400> SEQUENCE: 18
341 Glu Thr Leu Gln Phe Arg same
E--> 342 1 5
345 <210> SEQ ID NO: 19
346 <211> LENGTH: 8
347 <212> TYPE: PRT
348 <213> ORGANISM: artificial
350 <220> FEATURE:
351 <223> OTHER INFORMATION: upregulator of telomerase expression
353 <400> SEQUENCE: 19
355 Gln Tyr Ser Ile Gly Gly Pro Gln
E--> 356 1 5 same
359 <210> SEQ ID NO: 20
360 <211> LENGTH: 8
361 <212> TYPE: PRT
362 <213> ORGANISM: artificial
364 <220> FEATURE:
365 <223> OTHER INFORMATION: upregulator of telomerase expression
367 <400> SEQUENCE: 20
369 Ser Asp Arg Ser Ala Arg Ser Tyr

```

## RAW SEQUENCE LISTING

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Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\08082005\J511530.raw

E--> 370 1 5 *same*  
 373 <210> SEQ ID NO: 21  
 374 <211> LENGTH: 12  
 375 <212> TYPE: PRT  
 376 <213> ORGANISM: artificial  
 378 <220> FEATURE:  
 379 <223> OTHER INFORMATION: upregulator of telomerase expression  
 381 <400> SEQUENCE: 21  
 383 Asp Gly Asp Gly Asp Phe Ala Ile Asp Ala Pro Glu

E--> 384 1 5 10 *same*  
 387 <210> SEQ ID NO: 22  
 388 <211> LENGTH: 5  
 389 <212> TYPE: PRT  
 390 <213> ORGANISM: artificial  
 392 <220> FEATURE:  
 393 <223> OTHER INFORMATION: upregulator of telomerase expression  
 395 <400> SEQUENCE: 22  
 397 Asn Gly Asn Gly Asp

E--> 398 1 5 *same*  
 401 <210> SEQ ID NO: 23  
 402 <211> LENGTH: 5  
 403 <212> TYPE: PRT  
 404 <213> ORGANISM: artificial  
 406 <220> FEATURE:  
 407 <223> OTHER INFORMATION: upregulator of telomerase expression  
 409 <400> SEQUENCE: 23

E--> 412 Asp Gly Asn Gly Asp *use lower-case "l", not numeral "1"*  
 E--> 413 1 5 *same*  
 414 <210> SEQ ID NO: 24  
 415 <211> LENGTH: 5  
 416 <212> TYPE: PRT  
 417 <213> ORGANISM: artificial

W--> 418 <220> FEATURE:  
 419 <223> OTHER INFORMATION: upregulator of telomerase expression  
 421 <400> SEQUENCE: 24  
 422 Asn Gly Asp Gly Asp

E--> 423 1 5 *same*  
 434 <210> SEQ ID NO: 26  
 435 <211> LENGTH: 6  
 436 <212> TYPE: PRT  
 437 <213> ORGANISM: artificial

W--> 438 <220> FEATURE:  
 439 <223> OTHER INFORMATION: upregulator of telomerase expression  
 441 <400> SEQUENCE: 26  
 443 Asp Gly Asp Gly Phe Ala

E--> 444 1 5 *same*  
 460 <210> SEQ ID NO: 28  
 461 <211> LENGTH: 6  
 462 <212> TYPE: PRT



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Output Set: N:\CRF4\08082005\J511530.raw

463 <213> ORGANISM: artificial  
W--> 464 <220> FEATURE:  
465 <223> OTHER INFORMATION: upregulator of telomerase expression  
W--> 466 <400> SEQUENCE: 28  
468 Asp Gly Asn Gly Phe Ala  
E--> 469 1 5 *same*  
487 <210> SEQ ID NO: 31  
488 <211> LENGTH: 18  
489 <212> TYPE: DNA  
490 <213> ORGANISM: artificial  
W--> 491 <220> FEATURE:  
492 <223> OTHER INFORMATION: reverse primer for use in telomerase assay  
W--> 493 <400> SEQUENCE: 31  
494 ctaaccctaa ccctaacc 18  
E--> 495 *delete*

**RAW SEQUENCE LISTING ERROR SUMMARY**

DATE: 08/08/2005

PATENT APPLICATION: US/10/511,530

TIME: 09:54:57

Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\08082005\J511530.raw

**Invalid <213> Response:**

Use of "Artificial" only as "<213> Organism" response is incomplete,  
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27

Seq#:28,29,30,31

## VERIFICATION SUMMARY

DATE: 08/08/2005

PATENT APPLICATION: US/10/511,530

TIME: 09:54:57

Input Set : A:\PTO.YE.txt

Output Set: N:\CRF4\08082005\J511530.raw

L:9 M:283 W: Missing Blank Line separator, <130> field identifier  
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:30 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1  
L:44 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2  
L:56 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3  
L:61 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3  
L:64 M:283 W: Missing Blank Line separator, <220> field identifier  
L:65 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3  
L:68 M:283 W: Missing Blank Line separator, <220> field identifier  
L:85 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0  
M:332 Repeated in SeqNo=3  
L:100 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:4  
L:114 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:5  
L:128 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:6  
L:142 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:7  
L:156 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:8  
L:170 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:9  
L:192 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0  
M:332 Repeated in SeqNo=10  
L:207 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:11  
L:230 M:283 W: Missing Blank Line separator, <220> field identifier  
L:234 M:283 W: Missing Blank Line separator, <220> field identifier  
L:246 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0  
M:332 Repeated in SeqNo=13  
L:300 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0  
M:332 Repeated in SeqNo=15  
L:315 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16  
L:329 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17  
L:342 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:18  
L:356 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:19  
L:370 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:20  
L:384 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:21  
L:398 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:22  
L:412 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1  
L:413 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:23  
L:418 M:283 W: Missing Blank Line separator, <220> field identifier  
L:423 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:24  
L:428 M:283 W: Missing Blank Line separator, <220> field identifier  
L:430 M:283 W: Missing Blank Line separator, <400> field identifier  
L:438 M:283 W: Missing Blank Line separator, <220> field identifier  
L:444 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:26  
L:464 M:283 W: Missing Blank Line separator, <220> field identifier  
L:466 M:283 W: Missing Blank Line separator, <400> field identifier  
L:469 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:28  
L:474 M:283 W: Missing Blank Line separator, <220> field identifier  
L:476 M:283 W: Missing Blank Line separator, <400> field identifier  
L:478 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:29  
L:483 M:283 W: Missing Blank Line separator, <220> field identifier

**VERIFICATION SUMMARY**

DATE: 08/08/2005

PATENT APPLICATION: US/10/511,530

TIME: 09:54:57

Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\08082005\J511530.raw

L:485 M:283 W: Missing Blank Line separator, <400> field identifier  
L:491 M:283 W: Missing Blank Line separator, <220> field identifier  
L:493 M:283 W: Missing Blank Line separator, <400> field identifier  
L:495 M:254 E: No. of Bases conflict, this line has no nucleotides.